

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGAATTTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCCTGC
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

MHKAGLLGLCARAWSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
 SRKQQNVDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
 SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
 TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
 AGIVSFLCSEDASYITGETVVVGGGTPSRL

amino acids 1-15

amino acids 183-186

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

amino acids 276-278

Species	Sex	Age	Weight (g)	Length (mm)	Wing (mm)	Tail (mm)	Culmen (mm)	Gape (mm)	Bill (mm)	Foot (mm)	Middle toe (mm)	Claw (mm)	Toe + claw (mm)	Weight (g)	Length (mm)	Wing (mm)	Tail (mm)	Culmen (mm)	Gape (mm)	Bill (mm)	Foot (mm)	Middle toe (mm)	Claw (mm)	Toe + claw (mm)
1	♂	Ad.	100	150	60	40	10	15	10	10	10	5	15	10	150	60	40	10	15	10	10	10	5	15
2	♀	Juv.	80	140	55	35	8	12	8	8	8	4	12	8	140	55	35	8	12	8	8	8	4	12
3	♂	Ad.	120	160	65	45	12	18	12	12	12	6	18	12	160	65	45	12	18	12	12	12	6	18
4	♀	Juv.	90	150	60	40	10	15	10	10	10	5	15	10	150	60	40	10	15	10	10	10	5	15
5	♂	Ad.	110	155	62	42	11	16	11	11	11	5	16	11	155	62	42	11	16	11	11	11	5	16
6	♀	Juv.	85	145	58	38	9	14	9	9	9	4	14	9	145	58	38	9	14	9	9	9	4	14
7	♂	Ad.	115	162	64	44	11	17	11	11	11	5	17	11	162	64	44	11	17	11	11	11	5	17
8	♀	Juv.	95	152	61	41	10	16	10	10	10	5	16	10	152	61	41	10	16	10	10	10	5	16
9	♂	Ad.	125	168	66	46	13	19	13	13	13	6	19	13	168	66	46	13	19	13	13	13	6	19
10	♀	Juv.	98	154	62	42	11	17	11	11	11	5	17	11	154	62	42	11	17	11	11	11	5	17
11	♂	Ad.	130	170	68	48	14	20	14	14	14	7	20	14	170	68	48	14	20	14	14	14	7	20
12	♀	Juv.	100	156	63	43	12	18	12	12	12	6	18	12	156	63	43	12	18	12	12	12	6	18
13	♂	Ad.	135	172	70	50	15	21	15	15	15	8	21	15	172	70	50	15	21	15	15	15	8	21
14	♀	Juv.	105	158	65	44	13	19	13	13	13	7	19	13	158	65	44	13	19	13	13	13	7	19
15	♂	Ad.	140	175	72	52	16	22	16	16	16	9	22	16	175	72	52	16	22	16	16	16	9	22
16	♀	Juv.	110	160	67	45	14	20	14	14	14	8	20	14	160	67	45	14	20	14	14	14	8	20
17	♂	Ad.	145	178	74	54	17	23	17	17	17	10	23	17	178	74	54	17	23	17	17	17	10	23
18	♀	Juv.	115	162	69	46	15	21	15	15	15	9	21	15	162	69	46	15	21	15	15	15	9	21
19	♂	Ad.	150	180	76	56	18	24	18	18	18	11	24	18	180	76	56	18						

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CAGGGGGCCGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCAGACTTTCTGGCTGCGCTGGAGGACGCC**AT**GGAGCAGTACAAACTGC
AGAGCGACCCGCTGCGTGAGCAGCAGGAGGAGATGGTGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCTTTGTGCCTCGACCTCATAC
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GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
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GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA
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GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCCTTCTCGGAACTGGAGATGCAGCTGGAGGAGCAGC
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GGGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAATGAAGATGAGCTCCACCTGGC
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GAGGAAC TGAGGCAGCGGGAGGCGGCTGAGCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG
CCTGCCCTGGAAC TTTGGGCCTTTGTCCAAGCCCCGCGGGAAC TGCGACGAGCCAGCCCGGGGATGA
TTGATGTCCGAAAAA CCCCCCTG**TAA**GCCCTCGGGGCAGACCCTGCCTTGAGGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCCTACCGCACACCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCCAAAGAACTGGACCCTCATTT
AACAAAATAATATGCAAATTCCCACCCTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCCTTGTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTTTAGGCGTAAATGGATGTGCTTGTAGTTACGGGGTTTG
GCCAAGAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAAAATCTTTGAAGGGAC

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPDGDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQVLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQORRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS
LRQEKDSLKQRLEIDGKLQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

[illegible][illegible]

Year	Country	Population	Area	Population Density	Area Density	Population Density	Area Density
1970	France	34,000,000	640,000	53	100	100	100
1970	Germany	22,000,000	357,000	62	100	100	100
1970	Italy	21,000,000	301,000	70	100	100	100
1970	Spain	20,000,000	505,000	40	100	100	100
1970	U.S.	205,000,000	3,797,000	54	100	100	100
1970	U.S.S.R.	241,000,000	17,075,000	14	100	100	100
1970	China	700,000,000	9,570,000	73	100	100	100
1970	India	548,000,000	2,973,000	185	100	100	100
1970	Japan	125,000,000	377,000	331	100	100	100
1970	South Korea	29,000,000	100,000	290	100	100	100
1970	North Korea	19,000,000	120,000	158	100	100	100
1970	China	700,000,000	9,570,000	73	100	100	100
1970	India	548,000,000	2,973,000	185	100	100	100
1970	Japan	125,000,000	377,000	331	100	100	100
1970	South Korea	29,000,000	100,000	290	100	100	100
1970	North Korea	19,000,000	120,000	158	100	100	100

LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSTRNRRHVLYP

amino acids 33-39, 70-76

Year	Month	Day	Time	Location	Observer	Remarks
1961	April	10	10:00	1000 ft	W. H. B.	1st
1961	April	11	10:00	1000 ft	W. H. B.	2nd
1961	April	12	10:00	1000 ft	W. H. B.	3rd
1961	April	13	10:00	1000 ft	W. H. B.	4th
1961	April	14	10:00	1000 ft	W. H. B.	5th
1961	April	15	10:00	1000 ft	W. H. B.	6th
1961	April	16	10:00	1000 ft	W. H. B.	7th
1961	April	17	10:00	1000 ft	W. H. B.	8th
1961	April	18	10:00	1000 ft	W. H. B.	9th
1961	April	19	10:00	1000 ft	W. H. B.	10th
1961	April	20	10:00	1000 ft	W. H. B.	11th
1961	April	21	10:00	1000 ft	W. H. B.	12th
1961	April	22	10:00	1000 ft	W. H. B.	13th
1961	April	23	10:00	1000 ft	W. H. B.	14th
1961	April	24	10:00	1000 ft	W. H. B.	15th
1961	April	25	10:00	1000 ft	W. H. B.	16th
1961	April	26	10:00	1000 ft	W. H. B.	17th
1961	April	27	10:00	1000 ft	W. H. B.	18th
1961	April	28	10:00	1000 ft	W. H. B.	19th
1961	April	29	10:00	1000 ft	W. H. B.	20th
1961	April	30	10:00	1000 ft	W. H. B.	21st
1961	May	1	10:00	1000 ft	W. H. B.	22nd
1961	May	2	10:00	1000 ft	W. H. B.	23rd
1961	May	3	10:00	1000 ft	W. H. B.	24th
1961	May	4	10:00	1000 ft	W. H. B.	25th
1961	May	5	10:00	1000 ft	W. H. B.	26th
1961	May	6	10:00	1000 ft	W. H. B.	27th
1961	May	7	10:00	1000 ft	W. H. B.	28th
1961	May	8	10:00	1000 ft	W. H. B.	29th
1961	May	9	10:00	1000 ft	W. H. B.	30th
1961	May	10	10:00	1000 ft	W. H. B.	31st

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
 TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
 AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG
 GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
 GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCC
 GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
 TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCGCGCCCGCGCTGCTACCCCTG
 CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGGCTCCCGGCTG
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 GCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
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 AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
 CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
 GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
 TGGGTCTCCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
 CCCGCAGGCGGAAGCCCTGGCCGCAGCCGCCAGGACGCGATTGGCCCCGGAACCTCGCGCCCA
 CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
 AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGGCCCTCGGCCTGCCCGTGCCT
 GTGCACCGAGGAGGGGCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
 TCCACGTGACACGAGCCAGTGCTGCCCAGTGAAGGAGAGGAAGAACTACTGCGAGTTCT
 CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG
 TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCAGACGGAGTGTGTGGACC
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FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

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AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL
CAQPECPRLLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCRRCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIDPAGREVKTDTECTICHCTYEETWTR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
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AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
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GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCACACCAGACAAATCG
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CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTATATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

[illegible]

CGACG**ATG**CTACGACGCGCCCGGCTGCCTCCTCCGGACCTCCGCTAGCGCCTGCCGCGGCCCTTGCTGCGGGCGCTGCTCTCGTCGCTTGC GCGCTGCTCTCTTCTAGAGCCGAGGGACCCCGGTGGCCTCGTCGCTCAGCCCCCTATTTCCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATGTGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGCTGGTTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCTGAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCATGGATAGCAGCGCCGCCTTCCTGCAGGGGCTGTGGCAGCACTACCACCCTGGCTTGCCGCCGCCGGACGTTCGAGATATGGAGTTTGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTGATCACTGTGAGAAGTTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTTATCACGTGGAAGCCTTCAAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTACCTGTTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGCATAGATGATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAAGAGGATATGGGTATACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGAACAAGCAGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATGCAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTTGTACCTTATGCTCTCGAACCTGATATTTGTGCTTTTACCAGTGTGAAAATGCTAAGACTCCTAAAGAACAATTCCGAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTAT**AG**TAAGTAACTGAAGAACATTTTTAATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAAACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCCTCCTACTTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTCATAATAACACTTGAAAAGTGCTGGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACCTTTACAGATTGTTCTGCAGTTCTCTCTTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTTCTTAATCAGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAATTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAAAGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTTTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTAATTATATGTTTGGACAATTAGCAACAAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCATTCTGTCACTTGGCTTCGATTTTTTATATTTTCTATTATATGAAATGTATCTTTGGTTGTTTGATTTTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAATAAAGAAAATTCCTTGCTGACTTTAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSFYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCFSLAIGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCCTGACTTCTTCCCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTTGCACTATTACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGTCAGAAAATCTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAAATGACCGCAAGGAAATTTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCCTGCCCACGGATT
CCAGAGCCAATCCCAGATTTTCGCAATTTCTTCTTTCCACTTAAACTCTGAAAACAGGCACCTTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTTGGCGGAATTTATTTGGGGGGTCTGGTTGTCTTGTCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAAACCTCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCCTGATTTCCGCGATGAGTATTAGG
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTGTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAGAAAATGGAT
CCCCTGTTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTCCAGTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCTGATGGCATCCTGGATGCTTAGCATGCAAGTTT
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTAAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAAC
CTCATTTATAAAAGCTTCAAAAAAACCCA

[illegible]

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><subunit 1 of 1, 310 aa, 1 stop
```

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVPCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide:

Transmembrane domain:

N-glycosylation sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

amino acids 69-77

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

[illegible]

CAGGACCAGGTCCTTCCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCACTGCCACC GCCTTCTTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCCCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG
 TTCGTGCAGTCTGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTCTGGACCAGGCAGTGGCCCCAC
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
 GGCGCCTCCGGAGGCCAGACTTTTCCACTCCTTGCTCACAGCCTCCCCTGCCGCCCGGCCGAGACAGCACAGAGGCCA
 CCCAAACC¹AAAGAGCAGCCCAGAGCAGCCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTC
 GGCCCTGAGGACGACCTGGCTGGCATGTTCCCTCCAGATTTTCCCCTCAGCCCCGGACCCCTCGGTGGCAGAGCTC
 AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTCGTCCAGGGCAGCCCC
 GAGGTGCCGGGCATCACGGTGCCTGCTCCTGCAGGCCCTCGCCACCTGCTCAGCTCCCCACACGGCGGTGCCCTG
 GTGATGTCCATCAGCCGTAGCCACTTCTTGGCCTGCCCTGCTGCTGCAGTCTGCTGCAGTACCAGCGCTGTGTG
 CCACAGGACACCGGCTTCTCCTCCTCTCTGAAGTGCCTCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCCGGGCGAGGCTCAGTGAT
 GTGCGAGGGGGGCTCCTGCGCCTGGCCGAGGCCCTGGCCTTCCGTCAGGACCTGGAGGTGGTCAGCTCCACCGTC
 CGTGCCGTCTATCGCCACCTTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGACCTGATCAGCAAAGTCTCTCCAG
 GGGCTGATCGAGGTGAGGTCCCCCACCCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
 TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCTTGGCTGGG
 GGGAAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCCCTCGTCAGGCCCTCCTAGTGGACTGG
 CTGGAAATGCTGGACCCCGAGGTGGTTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG
 GGCAAAGGTCAGGCCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCTCTTTCACGCATCAGTCCAGCTGGCCC
 ACACTGCACCAAGTGCATCCGAGTCTCTGCTGGGCAAGAGCCGGGAACAGAGGTTTCAGCCCCCTCTGCCTCTCTGGAC
 TTCTCTTGGGCCCTGCATCCATGTTCTCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAAGCGGCGGGAG
 GAGCTGGTGTCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
 AGCCAGGACGGGGACACAGCCGCCCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTCAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGTGGCCGAGACCTTCTCTTCGAGCTCTTACCTACAGCGCCGGAGCTGCGGGTGGCCGTGCCCTGAGGTCTTA
 CTGCAAGCAGCGAAGGGCTGCCAGCAGCAGCGCTGCGAAGCTGGACGGACTCATCCACCGCTTCATCACGCTCCTT
 GCGGACACCGAGCACTCCCGGGCGTTGGAGAACCAGGGGCGGATGCCAGCATGCGCTGCCGGAAGCTGCGGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCTCTGCAGGCCGACCCACCTCAACTTC
 CAGGAGTTCCGGCAGCAGAACCCACCTGAGCTGCTTCTTGACAGTGTGGGCCCTGCTGGAGCTGCTGCAGCCGCAC
 GTGTTCCGCGAGCGAGCACAGGGGGCGCTGTGGGACTGCCCTTCTGTCTTCATCCGCCCTGCTGCTGAATTACAGG
 AAGTCTTCCCGCCATCTGGCTGCCCTTCATCAACAAGTTTGTGCAAGTTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCCTTCTCTGCAGAAAGCACGCCGACCCGCTCCACGACCTGTCTTTCGACAACAGTGACCTGGTG
 ATGCTGAAATCCCTCCTTGCAGGGCTCAGCCTGCCCAGCAGGACGACAGGACCGACCGAGGCCCTGGACGAAGAG
 GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTGCAGCTCTCCCTGTTTACCCCTCTGACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTGTCGCGCAACCTCGCCTTCAGCCTGGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTCAGCCGCTTTC
 CTGCCCACGTTTCATGTACTGCCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCCTGAG
 TACGCTCTCCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCCAAGCCCCGGCCGCTCCCGTCCCCGGGGATCCTCGAGGCCAAAGCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCACAGGCCAATACTCCGAGCCCTGGGGTGG
 CTCCGGGCCGCGCGCTGGCATCAGGGGCCGTGAGCCAAGCCCTCATTACCTTCTGGGCCAGCCCTGCCGCGG
 AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRLM
IRSEVLRLVDAALQDLEPQQQLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLQLQMLQWLDSFG
VEGGPLRAQLRMLASQASAGRRSLDVRGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPFPAKPVVVVSSLLLQEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIQVLLGKSREQRFDPASLDFLWACIHVPRIWQGRDQRTPOKR
REELVLRVQGPPELISLVELILAEAEATRSQDGDTAACSLIQARLPLLLSCCGDDESVRKVTE
HLSGCIQQWGDSVLGRRCRDLLLQLYLQRPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPIMIAALLHGRTHLNFQEFROQNHL
SCFLHVLGLLELLQPHVFRSEHQALWDCLLSFIRLLLNRYKSSRHAAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL
MSSAECCRNLAFLALRSMQNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE
HAAVLLHRAFLVGMYGMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

[illegible]

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FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGQGRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLLEVISPSPHFYPDFSRRLRESFGDPKERVVRWRTKQNLD
YCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515